

On a species survival model

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Abstract

In this paper we provide some sharp asymptotic results for a stochastic model of species survival recently proposed by Guiol, Machado, and Schinazi.

1 Introduction and statement of results

Recently, Guiol, Machado, and Schinazi [7] proposed a new mathematical framework for modeling species survival which is closely related to the discrete Bak-Sneppen evolution model. In the original Bak-Sneppen model [3] a finite number of species are arranged in a circle, each species being characterized by its location and a parameter representing the *fitness* of the species and taking values between zero and one. The number of species and their location on the circle are fixed and remain unchanged throughout the evolution of the system. At discrete times $n = 0, 1, \dots$, the species with the lowest fitness and its two immediate neighbors update simultaneously their fitness values at random. The Bak-Sneppen evolution model is often referred to as an “ecosystem” because of the local interaction between different species. The distinguishing feature of the model is the emergence of self-organized criticality [1, 2, 6, 8] regardless the simplicity and robustness of the underlying evolution mechanism. The Bak-Sneppen model has attracted significant attention over the past few decades, but it has also been proven to be difficult for analytical study. See for instance [6] for a relatively recent survey of the model.

The asymptotic behavior of the Bak-Sneppen model, as the number of species gets arbitrarily large, was conjectured on the basis of computer simulations in [3]. It appears that the distribution of the fitness is asymptotically uniform on an interval $(f_{\text{crit}}, 1)$ for some critical parameter f_{crit} , the value of which is close to $2/3$ [1, 8].

Guiol, Machado, and Schinazi [7] were able to prove a similar result for a related model with a stochastically growing number of species. Their analysis is based on a reduction to the study of a certain random walk, which allows them to build a proof using well-known results from the theory of random walks. The main result of [7] is

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thus based on general properties of Markov chains, and suitable variations of the result can in principle be carried out to other similar models.

In this paper we focus on the model introduced in [7] as is. Our aim is to elucidate the underlying mechanism responsible for the phenomenon described in [7] by sharpening the estimates that lead to the major qualitative statement therein. We proceed with a description of the Guiol, Marchado, and Schinazi (GMS) model.

In contrast to the Bak-Sneppen model, the number of species in the GMS model is random and changes in time, and only the species with the lowest fitness is randomly replaced. The local interaction between species is not considered in the GMS model, and therefore the spatial structure of the population is of no importance. Let $p > \frac{1}{2}$ be given and denote $q = 1 - p$. Let \mathbb{Z}_+ denote the set of non-negative integers and let $X = (X_n : n \in \mathbb{Z}_+)$ be a discrete-time birth and death process with the following transition probabilities: from each site, X_n increases by 1 with probability p ; from each site different than 0, X_n decreases by 1 with probability $q = (1 - p)$; finally, at 0, X_n stays put with probability q . Thus X is a nearest-neighbor transient random walk on the integer lattice \mathbb{Z}_+ with holding times and reflection barrier at zero. Throughout the paper we assume that $X_0 = 0$ with probability one.

The model describes the evolution of a population of species: newborn species are given "equal opportunity" by assigning them a random fitness, and the least fit species are the first to die. A jump to the right represents birth of a new species, whereas a jump to the left represents death of an existing species. Thus X_n represents the number of *species alive* at time n . When a new species is born, it is assigned a *fitness*. The fitness is a uniform $[0, 1]$ random variable independent on the fitness of all previously born species as well as of the path of the process X . When X jumps to the left, the species with the lowest fitness is eliminated. We remark that, in a different context, a similar model was considered by Liggett and Schinazi in [9].

Fix $f \in (0, 1)$. We examine the model by considering two coupled random processes, $L = (L_n : n \in \mathbb{Z}_+)$ (for *lower or left*) and $R = (R_n : n \in \mathbb{Z}_+)$ (respectively, for *right*), where L_n denotes the number of species alive at time n whose fitness is less than f while R_n denotes the number of the remaining species alive at time n .

Observe that L_n increases by 1 if X_n does and the newborn species has fitness less than f , and L_n decreases by 1 whenever X_n decreases by one and L_n is not zero. The value of L_n remains unchanged when either X_n increases by 1 and the newborn species has fitness at least f or X_n decreases by 1 and $L_n = 0$.

Notice that when it is not at zero, the process L evolves as a nearest-neighbor random walk with probability pf of jumping to the right, probability q of going to the left, and probability $1 - pf - q$ of staying put. When at zero, L_n jumps to the right with probability pf , and stays put with the complementary probability $1 - pf$. Thus L is a Markov chain. Since $p > q$, it is positive recurrent if $pf < q$, null-recurrent if $pf = q$, and is otherwise transient. In what follows we will denote the critical value q/p of the parameter f by f_c .

Consider the process $B = (B_n : n \in \mathbb{Z}_+)$, where B_n is the total number of species born by time n with fitness at least f . Observe that B is a non-decreasing Markov chain (formed by sums of i.i.d. Bernulli variables), which jumps one step up with probabilities $p(1 - f) = p - q$ and stays put with the complementary probability $2q$. It

is shown in [7] that when $f = f_c$, we have that for any $\varepsilon > 0$

$$0 \leq \limsup_{n \rightarrow \infty} \frac{B_n - R_n}{n^{1/2+\varepsilon}} \leq \frac{2}{q}, \quad \text{a.s.}, \quad (1)$$

while each species with fitness less than the critical value disappears after a finite (random) time. It follows from (1) that the distribution of species with fitness higher than f_c approaches a uniform law.

We sharpen the above result by proving the following theorem. Recall that $f_c = q/p$.

Theorem 1. *Suppose that $f = f_c$. Then*

1. $\limsup_{n \rightarrow \infty} \frac{B_n - R_n}{\sqrt{4qn \ln \ln n}} = 1, \quad \text{a.s.}$
2. $\frac{B_n - R_n}{\sqrt{2qn}} \Rightarrow |N(0, 1)|$, where $N(0, 1)$ denotes a mean-zero Gaussian random variable with variance one, and \Rightarrow stands for convergence in distribution.
3. $(L_n : n \in \mathbb{N})$ is a recurrent Markov chain (visiting zero infinitely often) and hence each species with fitness less than the critical value becomes eventually extinct with probability one.

The proof of the theorem is included in Section 2. Notice that by the law of large numbers $B_n \sim n(1 - f_c)$, a.s., as $n \rightarrow \infty$. Moreover, the fitness of any randomly chosen species from B_n is distributed uniformly on $(f_c, 1)$. Hence the theorem implies that this uniform law on $(f_c, 1)$ is the limiting distribution for the fitness of a randomly chosen species being alive at time n and having fitness larger than f_c .

2 Proof of Theorem 1

There is no loss of generality assuming that X is obtained recursively from an i.i.d. sequence of Bernoulli random variables $J = (J_n : n \in \mathbb{Z}_+)$ with $P(J_n = 1) = q$, $P(J_n = 0) = p$, as follows: $X_0 = 0$ and for $n \in \mathbb{Z}_+$ we have

$$X_{n+1} = X_n + (1 - J_n) - J_n(1 - s_n), \text{ where } s_n := \mathbf{1}_{\{X_n=0\}}. \quad (2)$$

Let $G = (G_n : n \in \mathbb{Z}_+)$ be a Markov chain formed by the pairs $G_n = (L_n, J_n)$. Figure 1 illustrates the transition mechanism of G .

2.1 Reduction from $B_n - R_n$ to an occupation time of G

Let $\Delta = (\Delta_n : n \in \mathbb{Z}_+)$ be the process defined through $\Delta_n = B_n - R_n$. Notice that Δ_n increases by 1 if and only if R_n decreases by 1, and otherwise stays put. That is

$$\Delta_{n+1} - \Delta_n = \mathbf{1}_{\{X_{n+1} - X_n = -1\}} \mathbf{1}_{\{L_n=0\}}.$$

Thus by (2), $\Delta_{n+1} - \Delta_n = (1 - s_n)J_n \mathbf{1}_{\{L_n=0\}}$, and we have

$$\Delta_n = \sum_{i=0}^{n-1} (1 - s_i)J_i \mathbf{1}_{\{L_i=0\}} = \eta_n - \sum_{i=0}^{n-1} J_i s_i, \text{ where } \eta_n := \sum_{i=0}^{n-1} J_i \mathbf{1}_{\{L_i=0\}}.$$

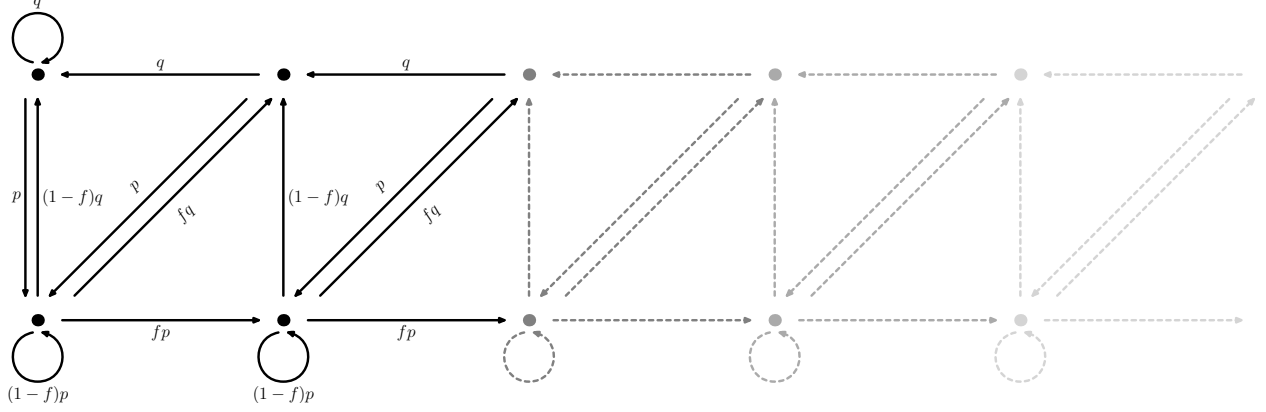


Figure 1: Transition probabilities for G

Observe that η_n is the occupation time (number of visits) of G at $(0, 1)$ up to time $n-1$ and that $\sum_{i=0}^{n-1} s_i J_i$ is bounded above by $\sum_{i=0}^{\infty} s_i$. Since X is transient and $X_0 = 0$, the latter series can be represented in the form $\sum_{i=0}^{\infty} s_i = \sum_{i=1}^g h_i$, where g is the total number of visits to zero (distributed geometrically, according to $P(g = k) = f_c^{k-1}(1 - f_c)$, $k \in \mathbb{N}$, see for instance [5, p. 274]) and h_i are successive holding times of X at zero (i.i.d. sequence of geometric random variables, independent of g , with $P(h_i = k) = q^{k-1}p$, $k \in \mathbb{N}$). In particular,

$$E\left(\sum_{i=0}^{\infty} s_i J_i\right) \leq E(g) \cdot E(h_1) = \frac{1}{p(1 - f_c)} = \frac{1}{2p - 1} < \infty.$$

Since L and consequently G are recurrent (and thus Δ_n is a non-decreasing sequence converging to $+\infty$ with probability one), it therefore suffices to show that Theorem 1 holds with $\Delta_n = B_n - R_n$ replaced by η_n in its statement.

Excursion decomposition for the path of L . We decompose the path of L into a sequence of successive excursions from 0, each one lasting until (but not including) the first time L returns to 0 from 1. Observe that once the Markov chain L is at zero, it will stay put until $J_k = 0$ and the fitness of the newborn particle is less than f_c . Therefore, the holding time of L at zero during one excursion is a geometric random variable with parameter $pf_c = q$. Let \tilde{h}_k be the i.i.d. sequence of holding times at zero during successive excursions of L from zero. That is, $P(\tilde{h}_k = n) = p^{n-1}q$, $n \in \mathbb{N}$. In what follows we will use the notation $\text{Geom}(a)$ for the geometric distribution with parameter a (for instance, we could write $\tilde{h}_k \sim \text{Geom}(q)$). Let σ_k be the k -th excursion starting time, that is $\sigma_1 = 0$ and

$$\sigma_k = \inf\{n > \sigma_{k-1} : X_{n-1} = 1, X_n = 0\}, \quad k = 2, 3, \dots$$

Define

$$\mu_k = \sum_{i=\sigma_k}^{\sigma_{k+1}-1} J_i \mathbf{1}_{\{L_i=0\}} = \sum_{i=\sigma_k}^{\sigma_k + \tilde{h}_k - 1} J_i \mathbf{1}_{\{L_i=0\}}.$$

Notice that $(\mu_k : k \in \mathbb{N})$ is an i.i.d. sequence and

$$\sum_{k=1}^{N_n} \mu_k < \eta_n \leq \sum_{k=1}^{N_n+1} \mu_k. \quad (3)$$

We now compute $\mu := E(\mu_k)$ using the fact that the sequence of pairs $G_n = (J_n, L_n)$ forms a Markov chain, the transition mechanism of which is illustrated in Fig. 1. The value of μ is equal to the expected number of visits by this Markov chain to the state $(0, 1)$ during the period of time starting at the state $(0, 1)$ with probability q and at $(0, 0)$ with probability p , and lasting until G leaves the set $\{(0, 0), (0, 1)\}$. We thus have, using first step analysis,

$$\mu = q(1 + \mu) + p(1 - f_c)\mu + pf_c \cdot 0 = q + \mu(1 - pf_c) = q + \mu p.$$

Hence $\mu = 1$. Consequently, using (3) and the law of large numbers, we obtain

$$\eta_n \sim N_n \text{ as } n \rightarrow \infty, \quad \text{a.s.} \quad (4)$$

Reduction to a simple random walk The duration of the k -th excursion of L from zero is equal to the sum $\tilde{h}_k + \alpha_k$ of the holding time at zero \tilde{h}_k distributed as $\text{Geom}(q)$, and the time α_k that it takes for L to return from 1 to zero. Notice that

$$\alpha_k = \sigma_k - (\sigma_{k-1} + \tilde{h}_k - 1).$$

For $m \in \mathbb{N}$ let $V_m = \sum_{k=1}^m (\tilde{h}_k + \alpha_k)$ be the total duration of the first m excursions of L from 0. Then $N_k = \max\{m : V_m \leq k\}$. With each excursion we can associate a *skeleton*, which is the path obtained from the excursion by omitting all transitions from a state to itself, for all states. If we let τ_k denote the length of the skeleton, then due to the choice of f_c it follows that τ_k has the same distribution as the time required for the simple symmetric random walk on \mathbb{Z} to get back to 0 starting from 0. Furthermore, the time spent by L at each visit to a site is a geometric random variable, $\text{Geom}(2q)$ for sites different than 0 and $\text{Geom}(q)$ for 0. Therefore, the length of a single excursion itself is a sum of one $\text{Geom}(q)$ random variable plus a sum of $\tau_k - 1$ independent $\text{Geom}(2q)$ random variables. If we replace \tilde{h}_k with a $\text{Geom}(2q)$, then the resulting modified “excursion time” becomes a sum of τ_k copies of a $\text{Geom}(2q)$ random variable. Let V'_m denote the total length of the first m excursions modified in this way. Let N'_k denote the number of such excursions occurred by time k , that is $N'_k = \max\{m : V'_m \leq k\}$. Then V_m stochastically dominates V'_m . By the law of large numbers,

$$\lim_{m \rightarrow \infty} \frac{V_m - V'_m}{m} = E(\tilde{h}_1) - E(h'_1) = \frac{1}{2q}, \quad (5)$$

where h'_1 is a geometric random variable with parameter $2q$. Letting $T_m = \sum_{k=1}^m \tau_k$, we obtain

$$V'_m = \sum_{k=1}^{T_m} h''_k,$$

where $(h_k'' : k \in \mathbb{N})$ is an i.i.d. sequence of random variables, each one distributed as $\text{Geom}(2q)$. Thus, by the law of large numbers,

$$V_m' \sim \frac{T_m}{2q} \text{ as } m \rightarrow \infty, \quad \text{a.s.} \quad (6)$$

Notice that T_m is distributed the same as the total length of the first m excursions from zero of a simple symmetric random walk.

2.2 Completion of the proof: CLT and LIL for η_n

LIL for η_n We need the following result. Although the claim is a “folk fact”, we give a short proof for the sake of completeness.

Lemma 1.

$$\liminf_{m \rightarrow \infty} \frac{T_m}{m^2/(2 \ln \ln m)} = 1 \text{ a.s.}$$

Proof of Lemma 1. Let $S = (S_n : n \in \mathbb{Z}_+)$ denote the simple symmetric random walk on \mathbb{Z} . Let $\gamma_0 = 0$ and define inductively $\gamma_{m+1} = \inf\{k > \gamma_m : S_k = m+1\}$. Let $Y_m = \gamma_{m+1} - \gamma_m$ with the usual convention that the infimum over an empty set is $+\infty$. Let $\phi(x) = \sqrt{2x \ln \ln x}$ for $x > 0$. By the law of iterated logarithm for S ,

$$\limsup_{n \rightarrow \infty} \frac{S_n}{\phi(n)} = \limsup_{n \rightarrow \infty} \frac{S_{\gamma_n}}{\phi(\gamma_n)} = \limsup_{n \rightarrow \infty} \frac{n}{\phi(\gamma_n)}.$$

Since $\phi^{-1}(x) \sim x^2/(2 \ln \ln x)$ as $x \rightarrow \infty$, we obtain

$$\liminf_{n \rightarrow \infty} \frac{\gamma_n}{n^2/(2 \ln \ln n)} = 1.$$

Observe that $\gamma_n = \sum_{i=0}^{n-1} Y_i$. The distribution of t_1 , the time to return to 0 starting from 0 for S , is equal to the distribution of t'_1 , the time to return to 0 starting from 0 for the reflected random walk $|S|$. Since t'_1 is equal in distribution to $1 + Y_1$,

$$\liminf_{m \rightarrow \infty} \frac{T_m}{m^2/(2 \ln \ln m)} = \liminf_{n \rightarrow \infty} \frac{\gamma_n + n}{n^2/(2 \ln \ln n)} = 1,$$

completing the proof of the lemma. □

Using the lemma along with (5) and (6), we obtain

$$\liminf_{m \rightarrow \infty} \frac{2qV_m}{m^2/(2 \ln \ln m)} = \liminf_{m \rightarrow \infty} \frac{2qV_m'}{m^2/(2 \ln \ln m)} = 1, \quad \text{a.s.}$$

Consequently, since N is the inverse of sequence of V , we obtain

$$\limsup_{k \rightarrow \infty} \frac{N_k}{\sqrt{4qk \ln \ln k}} = 1, \quad \text{a.s.}$$

Combining this with (4) completes the proof of the law of iterated logarithm for η_n .

CLT for η_n We now turn to the proof of the central limit theorem. It is well known (see for instance [5, p. 394]) that

$$\lim_{m \rightarrow \infty} E(e^{-\theta T_m/m^2}) = E(e^{-\sqrt{2\theta}}), \quad \theta \geq 0.$$

Therefore, it follows from (5) and (6) that

$$\lim_{m \rightarrow \infty} E(e^{-\theta V_m/m^2}) = \lim_{m \rightarrow \infty} E(e^{-\theta V'_m/m^2}) = E(e^{-\sqrt{\theta/q}}).$$

The function $\theta \rightarrow e^{-c\sqrt{2\theta}}$, $\theta \geq 0$, is the Laplace transform of a positive stable law with index $1/2$ whose density function is given by (see for instance [5, p. 395])

$$\varphi_c(u) = \mathbf{1}_{\{u \geq 0\}} \frac{ce^{-c^2/2u}}{\sqrt{2\pi u^3}}.$$

We intend to use this formula with $c = \frac{1}{\sqrt{2q}}$. Set $V_0 = 0$ and observe that for all $k \in \mathbb{N}$,

$$P(N_k \leq u) = P_0(V_{\lfloor u \rfloor} \geq k).$$

Fix $s > 0$ and let $u = \sqrt{k}s$. Then

$$P(N_k \leq \sqrt{k}s) = P(V_{\lfloor \sqrt{k}s \rfloor} \geq k) = P\left(\frac{V_{\lfloor \sqrt{k}s \rfloor}}{(\lfloor \sqrt{k}s \rfloor)^2} \geq \frac{1}{s^2}(1 + o(1))\right) \xrightarrow[k \rightarrow \infty]{} \int_{s^{-2}}^{\infty} \varphi_c(u) du.$$

Differentiating the right-hand side we obtain

$$\lim_{k \rightarrow \infty} P(N_k \leq \sqrt{k}s) = \int_0^s \frac{2e^{-u^2/(2c^{-2})}}{\sqrt{2\pi c^{-2}}} du.$$

Therefore N_k/\sqrt{k} converges weakly to the absolute value of a centered normal random variable with variance equal to $c^{-2} = 2q$. Combining this with (4) completes the proof of the central limit theorem for η_n . \square

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